

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:14:55 ; Search time 10069.4 Seconds
(without alignments)
3256.749 Million cell updates/sec

Title: US-09-227-881-2

Perfect score: 5304

Sequence: 1 atcttgctcagttacctc.....caggcacctcagcacagc 5304

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
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38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_est4a:*
42: em_estfun:*
43: em_esthum1:*

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45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
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65: em_estin3:*
66: em_estin4:*
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69: em_estov2:*
70: em_estp1:*
71: em_estp12:*
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86: em_estro12:*
87: em_estro13:*
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113: gb_gss22:*
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115: gb_gss24:*
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117: em_gss6:*
118: em_gss7:*
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121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.8	3.4	660	88	A0057239 CIT-HSP-2
2	179.8	3.4	539	96	A0379787 RPII-11-13
3	179	3.4	645	100	A0636457 RPII-11-4
4	179	3.4	678	96	A0387027 RPII-11-15
5	178.4	3.4	537	25	AW978041 EST390150
6	177.6	3.3	516	89	A0112451 CIT-HSP-2
7	177.4	3.3	577	91	A0265389 CITBI-E1
8	177.2	3.3	548	11	A1581291 tctb902.x
9	176.6	3.3	434	90	A0199435 RPII-11-58
10	176.6	3.3	591	25	AW979191 EST391301
11	176	3.3	521	21	AW273360 x138a04.x
12	176	3.3	551	39	T53829 yb585d10.s1
13	175.8	3.3	589	91	A0283440 RPII-11-79
14	175.4	3.3	386	98	A0474222 CITBI-E1
15	175.2	3.3	711	97	A0415030 RPII-11-2
16	175	3.3	388	19	AW069227 C141b09.x
17	175	3.3	421	23	AW674631 b41a11.x
18	175	3.3	447	24	AW820784 RC3-ST030
19	175	3.3	454	12	A1634187 t655a08.x
20	175	3.3	474	10	A1457313 t173a05.x
21	175	3.3	527	11	A1523813 q947c06.x
22	174.8	3.3	432	9	A1300818 q947c06.x
23	174.8	3.3	435	9	A1310992 q95a06.x
24	174.6	3.3	424	10	A1431513 t445f04.x
25	174.6	3.3	677	110	B66612 CIT-HSP-201
26	174.2	3.3	342	6	AA846823 oe06d01.s
27	173.8	3.3	565	110	B15692 345N8.TP.CT
28	173.8	3.3	565	25	AW953220 EST365290
29	173.6	3.3	368	21	AW270385 xp74f06.x
30	173.6	3.3	374	37	F35684 HSPD32531.H
31	173.4	3.3	384	5	AA862029 o146e04.s
32	173.4	3.3	427	5	AA550989 nj35d12.s
33	173.4	3.3	436	88	A0021084 CIT-HSP-2
34	173.4	3.3	486	8	A1049955 an38e01.x
35	173.4	3.3	642	110	B59854 CIT-HSP-345
36	173.4	3.3	836	102	A0781745 HS-3122.A
37	173.2	3.3	413	10	A1355246 qt74b06.x
38	173.2	3.3	430	10	A1859906 wmt3c01.x
39	173.2	3.3	508	100	A0632598 RPII-11-4
40	173.2	3.3	784	101	A0738890 HS-5382.B
41	172.8	3.3	496	4	AA486819 ab19c10.r
42	172.8	3.3	624	96	A0373399 RPII-11-15
43	172.6	3.3	300	7	AA937809 nw98b02.s
44	172.4	3.3	397	10	A1417469 t433b09.x
45	172.4	3.3	439	14	A1961983 wt41a12.x

ALIGNMENTS

RESULT 1
A0057239

LOCUS A0057239 660 bp DNA
DEFINITION CIT-HSP-2340D14.TP CIT-HSP Homo sapiens genomic clone 2340D14, DNA sequence.
ACCESSION A0057239
VERSION A0057239.1 GI:3353765
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 660)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
TITLE Unpublished (1998)
JOURNAL Other_GSSs: CIT-HSP-2340D14.TP
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2340D14"
/clone_1bp="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pbelOBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 116 a 188 c 150 g 206 t
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Query Match 3.4%; Score 180.8; DB 88; Length 660;
Best Local Similarity 86.0%; Pred. No. 2.4e-21;
Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;

Oy 1321 acctgagctacatgcgaacctctgcctccagggttcgaagcaattctctgtctcagctcc 1380
DB 293 attctacgctcactgcacacctctgcctccgggttcacgattctctgtcaccctcc 352
Oy 1381 cgcgtagctggagctcaaggcg-----cagcgccgctcaattttgttgtta 1432
DB 353 caagtagctggagattacgagccacacacacacacgcccggatattttgtttta 412
Oy 1433 gagatggggtttcacatattacccggctgtcttgaaaccttgacctgagtgatca 1492
DB 413 gngatggggtttcacatattacccggctgtcttgaaaccttgacctgagtgatca 472
Oy 1493 cccacctcagctcccttaagtgctgtggaattcaggaatgagtcacggccggcgaagg 1552
DB 473 cccacctcagctcccttaagtgctgtggaattcaggaatgagtcacggccggcgaagg 1552
Oy 1553 gtcagtgctt 1562
DB 533 ttttgtattt 542

RESULT 2
A0379787 539 bp DNA
LOCUS A0379787
DEFINITION RPII-152C3.TV RPII-11 Homo sapiens genomic clone RPII-11-152C3,

DNA sequence.
ACCESSION AQ379787.1 GI:4350810
VERSION AQ379787.1
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="GDB:7558034"
/db_xref="taxon:9606"
/clone="RPCI-11-152C3"
/clone_1ib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 187 a 112 c 123 g 116 t 1 others
ORIGIN
Query Match 3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity 76.8%; Pred. No. 3.6e-21;
Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;
OY 1280 agggtagaggtctgtgtctaacaccctacgtgtatgctctaaccttgagctcaactgcaacc 1339
DB 327 AGAGTCTCGCTGTCTCAGCAGGCTGAGTTCAGTGGCGGGATTTGGGCTCAGTGCACACC 268
OY 1340 tctgacctccagggtctcaagaattctctgtctcagacctcccggtgtagctgtagctacag 1399
DB 267 TCGGCTCCCGGGGTCAAGCAATTCCTGCTCAGCTCCCGAGTGTGCGGAGCAGCAG 208
OY 1400 gc-----gcacgcccgcgtcaattctgtatctgttaagtagagatgggtttacata 1451
DB 207 GCATGTGCCACATACCGCGCTAATTTTGTATTAGTAGAAGAACGGGGTTCACCATG 148
OY 1452 ttggccgggtgtgtctgaaacctctgacctcaagtgatcaaccacactcagccctccaaa 1511
DB 147 TTGGCCAGGCTGTGTAATCTCTGACCTCAGGTGATCCACCGCTTGGCTCTCTTAAA 88
OY 1512 gtctcgatctacagcatgagtcacgcgcgcgcgcaaggtgagtttaataagaa 1571
DB 87 GTGTGGGATTTACAGAGCTAGTACACACCGCGCGCTCAATCTTTTAAAGCTA 28
OY 1572 caactt 1577
DB 27 TGAATT 22

RESULT 3
LOCUS AQ636457/c 645 bp DNA GSS 17-JUN-1999
DEFINITION RPCI-11-465121.tj RPCI-11 Homo sapiens genomic clone RPCI-11-465121
DNA sequence.
ACCESSION AQ636457
VERSION AQ636457.1 GI:5099092
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:7678388"
/db_xref="taxon:9606"
/clone="RPCI-11-465121"
/clone_1ib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 214 a 118 c 139 g 174 t
ORIGIN
Query Match 3.4%; Score 179; DB 100; Length 645;
Best Local Similarity 88.2%; Pred. No. 4.8e-21;
Matches 209; Conservative 0; Mismatches 20; Indels 8; Gaps 1;
OY 1322 cctgagctcacgtcaacctctgctcccaaggtcaagcaattctctgtctcagctccc 1381
DB 248 CTTCAGCTCACTCAACCTCTGCTCCCAAGTTCAGTATTCCTGCTCAGCTCC 189
OY 1382 gcgttagctggtgactcaaggg-----cacgcccggcgaattttgtttgttagtag 1433
DB 188 GAGTAGCTGGGATTTACAGGGGTGTGTACACCGCCAGCTAATTTTGTATTAGTAG 129
OY 1434 agattgggttccaccatatagcccgagctgtcttgaaacctcgtgacctcagtgatccac 1493
DB 128 AGATGGGATTTACACATAGTTGGCCAGGCTGTCTCGACATCTCGACTCAAGTGAATGTC 69
OY 1494 ccacctcagctcttaagtctggtgattacagagcatgagtcacgcgcgcgcgcaaa 1550
DB 68 CCACCTCAGCTCCCAAGAGTGTGAGTTACAGCATGAGCCACCGCGCGCCGCAAA 12
RESULT 4
LOCUS AQ387027/c 678 bp DNA GSS 21-MAY-1999
DEFINITION RPCI11-153C12.tj RPCI-11 Homo sapiens genomic clone RPCI-11-153C12,

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
AF038702.1	GI:4358050	GSS	human.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	Zhuo, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building	Unpublished (1997)	Other GSS: RPCI11-153C12.TV Contact: Shaying Zhuo, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pdejong@omc.med.buffalo.edu). Clones may be purchased from BACpac Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html	Seq primer: SP6	Class: BAC ends.	Location/Qualifiers	1..678	/organism="Homo sapiens" /db_xref="GDB:7558427" /db_xref="taxon:9606" /clone="RPCI-11-153C12" /clone_11b="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC library"				
BASE COUNT	210 a	151 c	171 g	146 t					
ORIGIN									
Query Match	3.4%	Score 179:	DB 96:	Length 678:					
Best Local Similarity	77.4%:	Pred. No. 4.7e-21:							
Matches	233:	Conservative	0:	Mismatches	60:				
				Indels	8:				
				Gaps	1:				
1274	tcctgtagggtaagggctgtgtcttaacacctactgtatgtcttaacctagctact	1333							
1275		1334							
1276	tcagacacagagttctctctgtctgcacagcttgagagcagatctgcgctcaact	1335							
1277		1336							
1278	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1337							
1279		1338							
1280	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1339							
1281		1340							
1282	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1341							
1283		1342							
1284	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1343							
1285		1344							
1286	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1345							
1287		1346							
1288	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1347							
1289		1348							
1290	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1349							
1291		1350							
1292	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1351							
1293		1352							
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1295		1354							
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1297		1356							
1298	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1357							
1299		1358							
1300	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1359							
1301		1360							
1302	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1361							
1303		1362							
1304	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1363							
1305		1364							
1306	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1365							
1307		1366							
1308	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1367							
1309		1368							
1310	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1369							
1311		1370							
1312	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1371							
1313		1372							
1314	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1373							
1315		1374							
1316	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1375							
1317		1376							
1318	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1377							
1319		1378							
1320	gcaacctctgctccctccaggttaagaacattccctgtctcagaacctcccgctagctggga	1379							
1321		1380							

[illegible]

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Human sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 516) Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other GSSs: CIT-HSP-2372C9, TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdamas@tigr.org Clones are available from Research Genetics (Info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_11b="CIT-HSP" /sex="Male" /cell-type="Sperm" /note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.3%; Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 8,6e-21;
Matches 213; Conservative	0; Mismatches 29; Indels 8; Gaps 12;
OY	1321 acctgagctcactgtaaacctctgctccccaaggttcaagaattctctgctcagctcc 1380
Db	255 ATCTCATCTACATGCAACCTCTGCTCCCGGGTTCAAGGATTCTCTCAGACCTCC 314
OY	1381 cgcgtagctcgggaactacagcg-----cagcccgctaatattttatgttaagta 1432
Db	315 CAAGTAGCTGGGATTACAGCGCCACACACACACGCCCGCTAATTTTATTTTAAAGTA 374
OY	1433 ggaatggggattcacacatatagcccgagtggtgtctgtaacctctgacctcaggtgatca 1492
Db	375 GAGATGGGGTTTACACCATTTTGGCCAGCGCTGGTCTCGAATCTCTAGCTATGATCA 434
OY	1493 ccacactcagctctcaaaagtctggaattaaagcatagatgacacgcgcgcgccaagg 1552
Db	435 CCCACTTGCGCTCCCAAGGTGCTGGGATTACAGGCGCTGGCCACTGGCCCGAGCTAAT 494
OY	1553 gtcagtgctt 1562
Db	495 TTTTGCATTT 504
RESULT	7
LOCUS	A0265389 577 bp DNA GSS 27-OCT-1998
DEFINITION	CITBI-E1-2509010.TF CITBI-E1 Homo sapiens genomic clone 2509010, DNA sequence.
ACCESSION	A0265389
VERSION	A0265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 577) Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSS: CITBI-EI-2509010.TR Contact: Mark Adams The Institute of Eukaryotic Genomics 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: mdadams@ligr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.ligr.org/tldb/humgen/bac_end_search/bac_end_search.html . Seq primer: MI3-21 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..577 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2509010" /clone_id="CITBI-EI" /sex="male" /cell_type="sperm" /note="Vector: pBELBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
BASE COUNT	167 g 127 c 137 g 146 t
ORIGIN	
Query Match	3.3%; Score 177.4; DB 91; Length 577;
Best Local Similarity	75.1%; Pred. No. 9.1e-21;
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1;
Oy	1321 acctgagtcactcgaacctctgcctcccaaggctcaagaacaatttcctgcgtcacagccc 1380
Dd	
Dd	atctcgctcatcctaacccttgcctccccaagttaactgatgtttccctgcctcacagctcc 309
Oy	1381 ccgcgtagcttggaactacagagc-----gcagccccggctaatttgttatgttagta 1432
Dd	308 CGAGTATCTTAGGACTACACGCCACC GCCACCAAGCGCTGTGAATTTCGTAATTTTAAATA 249
Oy	1433 gagatgygggttcacacatatatagcccggtggtgcttgaaactctgcagctcagtgatcca 1492
Dd	248 GAGAGCGGGGTTTACACATGTTGCAGCGCTGCTGTGAACCTCTGACCTCAGCGCATCCA 189
Oy	1493 cccaactaacgctcctctaaagtgcgtgggtttacaggaatagatgaatcacgcggcccgcaagg 1552
Dd	188 CCCGCTTGCGCTCCCAAGAAGTCTGGGATTCAGGCATGAGCACCTGCACCCACGCCA 129
Oy	1553 gtccagttgtttaataagaataacttgaaatggtttactaaaccaacagggaaacagacaaa 1612
Dd	128 GATACATTTTGTGAATAATCTAGACTGGAACTCAGTGACACGCTCTCAGGCAAAAGGAGAAAT 69
Oy	1613 agctgtgataaatltcag 1629
Dd	68 AGTAACTAGGTATGAG 52
RESULT	8
LOCUS	A1583291/c
DEFINITION	A1583291 548 bp mRNA EST 14-DEC-1999
ACCESSION	t56gq2.x1 NCI CGAP HSC4 Homo sapiens CDNA clone IMAGE:2244818 3' similar to TR:Q13538 O13538 ORF2. FUNCTION UNKNOWN. contains Alu repetitive element., mRNA sequence. A1583291

VERSION	AT583291.1	GI:4569188
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 548)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bnpr/image/image.html Insert length: 664 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 664 POLYA-No.	

FEATURES	SOURCE
Location/Qualifiers	1. .548
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_image:224818"	
/clone_lib="NCI_CGAP_HSC4"	
/tissue_type="CD34+", CD38-	from normal bone marrow donor"
/lab_host="DH10B"	
/note="organ: bone marrow; Vector: pAMP1, mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. CDNA library Preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."	
BASE COUNT	150 a 136 c 129 g 133 t
ORIGIN	

Query Match	3.3%	Score 177.2	DB 11	Length 548:
Best Local Similarity	78.8%	Pred 9.9e-21:		
Matches	227:	Conservative	0:	Mismatches 53: Indels 8: Gaps 1
Oy	1277	gtgagggtgaggggtctgtgtgtcttaacactaactgtatgtctcttaacacctgagctactgca	1336	
Db	546	GAGGAGAGCTTGATGATGTGTGCTCAGGCTGAGAGGCGAGTGAGATCTTGCGCACTGGCA	487	
Oy	1337	acctctgtccctcccaagcttcaagcaattctctctgtctcaagctcccgctgaagctggagacta	1396	
Db	486	ACCTCGCGCTCAGACGTTTCAGACGATTTCTCTGCGCCCTCAGCCTCTCTAGCAGCTGAGACACTA	427	
Oy	1397	cagcgctg-----cagcgccgagctaaatttttgttatgtttagtagaagatggggtttcacc	1448	
Db	426	CAGCGCGCCCGCCACACACGCGCTGGCTAATTTTGTATTTTGTAGTAGAGATGGGGTTTTCACC	367	
Oy	1449	atatattgacccggagctgtgtcttgaacctcctgaacctcagtgatcatcaaccacactcaagctctct	1508	
Db	366	ATGTTGGCCAGGCGTGGTGTGGAATCTGACCTCAGCTATCCAGCTACCTGTTGTTGCC	307	
Oy	1509	aaagtgtctggagattacaaggacatgaatcacgcgcgcgcgcgaaggttca	1556	
Db	306	AAAGTGTGGGATTTACAGGATGAGGACACCGTGGCCAGCCAGGATTTTA	259	

RESULT	9			
A0199435/c				
LOCUS	A0199435	434 bp	DNA	GSS
				20-APR-1999

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
PC111-58F5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-58F5, DNA sequence.	A0199435	A0199435.1	GI:3611634	GSS.	human.					
					Homo sapiens					
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
					Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
					1 (bases 1 to 434)					
					Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,					
					Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.					
					Use of human BAC End sequences for Sequence-Ready Map Building					
					Unpublished (1998)					
					Other-GSS: RPCI11-58F5.TK					
					Contact: Mark Adams					
					Department of Eukaryotic Genomics					
					The Institute for Genomic Research					
					9712 Medical Center Dr., Rockville, MD 20850, USA					
					Tel: 301 838 0200					
					Fax: 301 838 0208					
					Email: madams@tigr.org					
					Clones are derived from the human BAC library RPCI-11. For BAC					
					library availability, please contact Pieter de Jong					
					(pieter@jong.med.buffalo.edu). Clones may be purchased from					
					BACpac Resources (http://bacpac.med.buffalo.edu/ordering) or from					
					Research Genetics (info@resgen.com). BAC end search page:					
					http://www.tigr.org/tcd/humans/bac_end_search/bac_end_search.html					
					Class: BAC ends.					

FEATURES	SOURCE
Location/Qualifiers	
1..434	
/organism="Homo sapiens"	
/db_xref="GDB:7522012"	
/db_xref="taxon:9606"	
/clone="RPC1-11-58F5"	
/clone_1kb="RPC1-11"	
/sex="Male"	
/cell_type="Lymphocytes"	
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library"	
118 a 108 c 114 g 94 t	

	Query Match	Similarity	3.3% 77.4%	Score 176.6	DB 90	Length 434
	Best Local	Similarity		Pred. No. 1,3e-20		
	Matches	230	Conservative	0	Mismatches 59	Indels 8
						Gaps 1
OY	1292	tggtgtctaacacctaacctgtatgtcctctaacaccytagctactgtcaacctctgcctccag	1351			
Db	427	tgtctactcagcctcgagagcgaatggcagacgacttggctctctgtgcaacctctgctcctgg	368			
OY	1352	gttcaagaacattccctctctccagaccctccgcgctagctcggagacacaagc-----gc	1403			
Db	367	gttcaagaacattctctcctctcagcctctccaaatagatgagattacagggcacccggccaac	308			
OY	1404	acgccccggtcaatttttgtagttttagtaagaatgagggtttcacacatatggccgcgtg	1463			
Db	307	atgcccgctcaattttttgtatatttttagtacgaatggggtttcactatctttggcctgcgcta	248			
OY	1464	gtcttgaacctctgaacctcagtgatccaaccacactcagcctctctaaagtgtcggatella	1523			
Db	247	gtcttggaacctcggagacctcagagtgatctacactggcttggcctctcgaagtgctggagatta	188			
OY	1524	caggaatagatcacccggcccgcccaagtgatcagtggttataataaggaataactcgaa	1580			
Db	187	cagggtgtatgctaccctgctccagcagcagagatgaggttttatcaggaaggaattctgaa	131			

RESULT	10
LOCUS	AW979191
DEFINITION	AW979191 501 bp mRNA EST391301 MAGE resequences, MAGP Homo sapiens CDNA, mRNA sequence.

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. 1 (bases 1 to 521)	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)
Contact: Robert Strausberg, Ph.D.	Tel: (301) 496-1550	Email: Robert_Strausberg@nih.gov	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.	CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.	DNA Sequencing by: Washington University Genome Sequencing Center	DNA distribution: NCI-CCAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.linn.gov/bdnp/image/image.html		
Possible reversed clone: polyT not found	Seq primer: -40UP from gibco	High quality sequence stop: 411.	Location/Qualifiers	
1..521	/organism="Homo sapiens"	/db_xref="taxon:9606"	/clone="IMAGE:2762382"	/clone_id="NCI-CCAP-U64"
/tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"	/lab_host="DH10B"	/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI. Cloned unidirectionally. Primer: Oligo dt.	Average insert size 1.48 kb. Life Technologies catalog #:	11542-016"
BASE COUNT	115 a	131 c	108 g	167 t
ORIGIN				
Query Match	3.3%	Score 176;	DB 21;	Length 521;
Best Local Similarity	80.7%	Pred. No. 1.6e-20;		
Matches 221;	Conservative 0;	Mismatches 45;	Indels 8;	Gaps 1;
QY 1321	accgagatcactcgaactctgctcccaagttcaagcaattctccgtctcagctcc	1380		
Db 56	ATCTCGCTCACTCAACACTCTGCTCCCAATTCACAGATTCCTCTGCTCAAGCTTC	115		
OY 1381	cgcctagcttggaactacagcg-----caagcccgcaattttgtattgtatga	1432		
Db 116	TGAGTAGCCAGGATTACAGGTGCCCCGACACACACAGCCAGCTAATTTTGTATTTTATA	175		
OY 1433	gagatgggttcacacatattagccggctggtcttgaaactctgaaactcagtgatcca	1492		
Db 176	GAGATGGGTTTCACTAATGTTGGCCAGAGCTAGTGTATCTGACCTCAGGTGATCCA	235		
OY 1493	cccaactaagcctcctaaagtgtctgggattacaggaatgattcaacggccggccgaag	1552		
Db 236	CCCCCTCAGCTCCCAAGTGTGGGATTCAGAGCAAGATCAACCGCCCTGGCCCTTC	295		
OY 1553	gtcagtgcttaataaggaataactggaatgttt	1586		
Db 296	CTGACTTTTGTAGTATCACTTCTAATCTGATAT	329		
RESULT 12				
LOCUS	T53829	551 bp	MRNA	EST
DEFINITION	Y085d10.s1 StrataGene liver (c937224) Homo sapiens cDNA clone IMAGE:77971 3' similar to contains 11 repetitive element, mRNA sequence.			
ACCESSION	T53829			
VERSION	T53829.1	GI:655690		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissee, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
'M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
'B., Morris, M., Parsons, J., Pange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierrey-Meg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.,
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
MEDLINE 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
COMMENT Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 760
High quality sequence stops: 380 Source: IMAGE Consortium, LIND. This
clone is available royalty-free through LIND; contact the IMAGE
Consortium (info@image.lind.gov) for further information.
Insert Length: 760 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 380.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/db_xref="GDB:497716"
/db_xref="taxon:9606"
/clone="IMAGE:77971"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOuR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'
BASE COUNT 119 a 134 c 127 g 163 t 8 others
ORIGIN
Query Match 3.3%; Score 176; DB 39; Length 551;
Best Local Similarity 80.7%; Pred. No. 1.6e-20;
Matches 221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;
OY 1321 accgaagcctcgaacctgcctcccgaggttcgaagaattctccctcgaagctcc 1380
DB 47 ACTCTGGCTCACTGCACACTCTGCTCCAGATTCAGAGATTCTCTCCCTCAGCTCC 106
OY 1381 cgcgtagctggaactaacagcg-----caagcccgagctaatcttgatgtagta 1432
DB 107 TGAGTAGCAGAGATTACAGAGTGCCTCCGACACACACCACTAATTTTGTATTAGTA 166
OY 1433 gagatgaggttccacatatgagcccgctggtcttgaaactccgaactcgaagtatcca 1492
DB 167 GAGATGGGGTTTCACTATGTTGGCCAGGCTAGCTTGTACTCTGACCTCAGGTGATCCA 226
OY 1493 ccacactcagctcctctaaagtctggaattacagcatagtcacagcgcccgagccaag 1552
DB 227 CCGGCTCAGCCTCCCAAGTGTCTGGATTACAGGCATAGTCACGCCCTGCGCTTTC 286
OY 1553 gtcaagtgttaataaggaataactggaatgttt 1586
DB 287 CTGACTTTTACTGATCACCATTCTAAGTAT 320

RESULT 13
AQ283440

LOCUS AQ283440 589 bp DNA GSS 27-APR-1999
DEFINITION RPEC11-79G5.TV RPEC1-11 Homo sapiens genomic clone RPEC1-11-79G5, DNA
sequence.
ACCESSION AQ283440
VERSION AQ283440.1 GI:3908257
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Baas, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.,
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
JOURNAL Other_GSSs: RPEC11-79G5.TV
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@ligr.org
Clones are derived from the human BAC library RPEC1-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.org/rdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1..589
/organism="Homo sapiens"
/db_xref="GDB:7530100"
/db_xref="taxon:9606"
/clone="RPEC1-11-79G5"
/clone_lib="RPEC1-11"
/sex="male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPEC11 Human Male BAC Library"
BASE COUNT 146 a 126 c 136 g 181 t
ORIGIN
Query Match 3.3%; Score 175.8; DB 91; Length 589;
Best Local Similarity 75.7%; Pred. No. 1.7e-20;
Matches 234; Conservative 0; Mismatches 67; Indels 8; Gaps 1;
OY 1280 agggtagaggtctggtcttaccactaccctgtagctctacacctgagctcactgaacc 1339
DB 105 AGAGTCTGCTCTGTGGCCAGCTGGAGTACAGTGGCGATGTCACACTCTACTCAAC 164
OY 1340 tctgctcccaaggttcaagcaattcctgltcagacctcccgctagctggaactaac 1399
DB 165 TCTGACTCTCTGGTTCAGACATCTCTGCTTAGCCCCCGAGTACTGGGATTACAG 224
OY 1400 gcg-----caagcccggtcatttttgatgttgtagtagagtggtttaccata 1451
DB 225 GTGCTGCACCACTATCGTAGCTAATTTTGTATTGTAGCACAGATGGGGTTTCACATA 284
OY 1452 ttagcccggtctgtcttaactccggaactcaggtgatccaccccccgaagctcctaa 1511
DB 285 TTGGTCAGGCTGTGTGTAATCTCTGACTCTATGTGATCCACCCCTCAGCTCCCAA 344
OY 1512 gtgctgggattcaagcatgagtcacgcccggccaaagggtcagtggttaataagaa 1571
DB 345 GTGCTGGGATTACAGCGGAGACCGACGTCGCTGTCCAGGGGATGATGTTTATAGAA 404
OY 1572 taacttgaa 1580
DB 405 TAATCTGCA 413

Db 65 CTTGCTCGTTTGTA 48

Search completed: December 3, 2000, 10:15:10
Job time: 1398 sec

• • • • •